

|   |  |      |     |      |    |
|---|--|------|-----|------|----|
| nitrogenase (EC 1.1.1.1)                    |  |      |     |      |    |
| hypothetical prote                          |  |      |     |      |    |
| proline-tRNA synth                          |  |      |     |      |    |
| cell surface glyco                          |  |      |     |      |    |
| cell surface glyco                          |  |      |     |      |    |
| conserved hypote                            |  |      |     |      |    |
| minor inner core P                          |  |      |     |      |    |
| DNA-directed DNA p                          |  |      |     |      |    |
| rotein T22H9.3 [1]                          |  |      |     |      |    |
| probable ligand-ga                          |  |      |     |      |    |
| exonuclease ABC C                           |  |      |     |      |    |
| ferrous iron trans                          |  |      |     |      |    |
| hypothetical prote                          |  |      |     |      |    |
| probable tRNA meth                          |  |      |     |      |    |
| hypothetical prote                          |  |      |     |      |    |
| probable merhanol                           |  |      |     |      |    |
| nicotinamide (NICM)B                        | 1  | 458  | 7.1 | 80.5 | 30 |
| T48830                                      | 2  | 231  | 7.0 | 80   | 31 |
| P70332                                      | 2  | 570  | 7.0 | 80   | 32 |
| B53434                                      | 2  | 296  | 7.0 | 79.5 | 33 |
| A54434                                      | 2  | 335  | 7.0 | 79.5 | 34 |
| A63415                                      | 2  | 501  | 7.0 | 79.5 | 35 |
| P44R8V                                      | 1  | 654  | 7.0 | 79.5 | 36 |
| DJBEB1                                      | 1  | 1240 | 7.0 | 79.5 | 37 |
| F88925                                      | 2  | 990  | 6.9 | 78.5 | 38 |
| C96493                                      | 2  | 933  | 6.9 | 78   | 39 |
| A83329                                      | 2  | 940  | 6.9 | 78   | 40 |
| D71909                                      | 2  | 642  | 6.8 | 77.5 | 41 |
| CB4488                                      | 2  | 970  | 6.8 | 77.5 | 42 |
| H97112                                      | 2  | 441  | 6.8 | 77   | 43 |
| T20338                                      | 2  | 294  | 6.7 | 76.5 | 44 |
| P725610                                     | 2  | 306  | 6.7 | 76.5 | 45 |
| GenCore version 5.1.6                       |  |      |     |      |    |
| Copyright (c) 1993 - 2005 Compugen Ltd.     |  |      |     |      |    |
| OM protein - protein search, using sw model |  |      |     |      |    |
| Run on:                                     | February 16, 2005, 16:16:11 ; Search time 9.04128 Seconds<br>(without alignments)<br>2330.584 Million cell updates/sec |      |     |      |    |
| Title:                                      | US-10-003-356-2  |      |     |      |    |
| Perfect score:                              | 1138   |      |     |      |    |
| Sequence:                                   | 1 MPERRKQDDEGPGIHEFLAF.....RVIASDKIQSKAVVRKRIQHF 219   |      |     |      |    |
| Scoring table:                              | BLOSUM62   |      |     |      |    |

Total number of hits satisfying chosen parameters:

AS6715      calcium receptor (clone rhbcrp-4) - human  
AS6716      calcium receptor (clone rhbcrp-5) - human

Post-processing: Minimum Match 0%  
Maximum Match 100%  
C:Species: Homo sapiens (man)  
C:Date: 19-Oct-1995 #Sequence revision 19-Oct-1995  
C:Accession: A56715; S49311; A49419; B4919; C49419  
C:Text\_Change 01-Dec-2000

LBCB RIRBT 4 b Summaries

1: Pir1,\*  
2: Pir2,\*  
A: Reference number: A\_56713; PMID: 7755551  
A: Reference number: A\_56713; PMID: 7755551

A;Status: preliminary  
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and  $\Delta$  is the difference between the score of the result being printed and the average score of the other results.

SUMMARIES  
A;Reference number: S49341  
A;Accession number: S49341

A;Status: preliminary

| No. | Score | Match      | Length | DB               | ID           | Description |
|-----|-------|------------|--------|------------------|--------------|-------------|
| 1   | 160   | /Q...A'981 | 1      | Residue          | 1-160        | <PBA>       |
| 2   | 160   | /Q...A'981 | 1      | Cross-references | EMBL:2811086 | A Cross-    |
| 3   | 160   | /Q...A'981 | 1      | Residue          | EMBL:2811086 | -reference  |

R; Pollak, M.R.; Brown, B.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steimann, Cell 75, 1297-1303, 1993

A:Reference: mutations in human CA(3)-B695C receptor gene cause familial myopathy. A:Reference number: A49419; PMID:7916660

A:Statins preliminary A:Statins preliminary  
A:Statins molecule two: DNA  
A:Statins molecule two:  
DNA

| 8 | 225.7 | 19.7 | 1210 | 2 | I42131 | metabotropic glutamate receptor 1B |
|---|-------|------|------|---|--------|------------------------------------|
| 9 | 225.5 | 19.8 | 908  | 2 | I49142 | metabotropic glutamate receptor 1A |
| 8 | 225.5 | 19.8 | 908  | 2 | I49142 | metabotropic glutamate receptor 1A |
| 9 | 225.5 | 19.8 | 908  | 2 | I49142 | metabotropic glutamate receptor 1A |

A Note: sequence extracted from NCBI backbone (NCBInI:1142453) A;Accession: B44119

|    |       |    |      |      | A;Molecule type: DNA         |
|----|-------|----|------|------|------------------------------|
|    |       |    |      |      | A;Molecule type: Preliminary |
|    |       |    |      |      | G Protein-coupled            |
|    |       |    |      |      | metabotropic Gluta           |
| 15 | 203.5 | 15 | 18.9 | 1199 | 2 JH0561                     |
| 16 | 203.5 | 16 | 17.9 | 877  | 2 JH1939                     |

298 Lys mutation is associated with familial hypocalciuric hypercalcemia (NCBI:142555)  
 298 Lys mutation is extracted from NCBI backbone  
 A; Note: sequence extracted from NCBI backbone  
 A; Note: probable ligand-gated ionotropic glutamate receptor  
 A; Note: hydantoinase  
 A; Note: 20 86.5 7.6 921 2 P84732  
 A; Note: 21 86.5 7.6 923 2 P84732

N; Accession: C43419  
N; Status: Preliminary

A; Note: sequence modified after extraction from NCBI backbone  
 A; Note: 796-797 mutation is associated with familial hypocalciuric hypercalcemia  
 A; Note: sequence extracted from NCBI backbone (NCBIDB:142457)

C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 31.0% Score 353; DB 2; Length 1078;

Best Local Similarity 37.1%; Pred. No. 7e-25; Gaps 5;

Matches 78; Conservative 44; Mismatches 64; Indels 24;

A:Accession: 18 LAFLW--AELGSEAKEKEERTCRLLGKCYDAENHSLVIGGLPFDSTRTIPANESI-LE 74

Db 11 LALTWHTSAYGPQRAQKGD-----ILLGGLFPFHFGVAAKQDLSR 54

Qy 75 PASAKCEGFNQFRMAMIMIKEINRKDILPNTLGYQIFDTCTSKSVEAVLYF 134

Db 55 PESVCTRYNFRGFWLQAMIFAEETINSPLLNPNTLGYRIFDTCTNSVKALETLSF 114

Qy 135 LTQGB--EIRPNERNSTGAFPA--GIVAGGGSFLSVPSARLGLYLYLPOGVYTSTCVIL 189

Db 115 VAQNKKDSNLNDEFNCNSEHIPSITIAVGATSGVSTAVANLGLFYIPQVSASSRL 174

Qy 190 SDKYQFPSPYLVIASDKIOSKAVVKRICHF 219

Db 175 SNKQPKSFSLRTLPNDHQATAMADIEYF 204

RESULT 2

B56715 calcium receptor (clone phPCaR-5.2) - human  
C;Species: Homo sapiens (man)  
C;Accession: B56715 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
C;Accession: B56715 R;Garrett, J.B.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.-I.; Brown, E.M.; Hebert, S.C.  
A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor  
A;Reference number: A56715; MUID:95279439; PMID:7759351  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Cross-references: GB:U20760; NID:9681746; PID:AAA06504.1; PID:9683747  
C;Keywords: Glycoprotein; receptor; transmembrane protein

Query Match 31.0% Score 353; DB 2; Length 1088;

Best Local Similarity 37.1%; Pred. No. 7e-25; Gaps 5;

Matches 78; Conservative 44; Mismatches 64; Indels 24; Gaps 5;

Qy 18 LAFLW--AELGSEAKEKEERTCRLLGKCYDAENHSLVIGGLPFDSTRTIPANESI-LE 74

Db 11 LALTWHTSAYGPQRAQKGD-----ILLGGLFPFHFGVAAKQDLSR 54

Qy 75 PASAKCEGFNQFRMAMIMIKEINRKDILPNTLGYQIFDTCTSKSVEAVLYF 134

Db 55 PESVCTRYNFRGFWLQAMIFAEETINSPLLNPNTLGYRIFDTCTNSVKALETLSF 114

Qy 135 LTQGB--EIRPNERNSTGAFPA--GIVAGGGSFLSVPSARLGLYLYLPOGVYTSTCVIL 189

Db 115 VAQNKKDSNLNDEFNCNSEHIPSITIAVGATSGVSTAVANLGLFYIPQVSASSRL 174

Qy 190 SDKYQFPSPYLVIASDKIOSKAVVKRICHF 219

Db 175 SNKQPKSFSLRTLPNDHQATAMADIEYF 204

RESULT 3

15362 calcium/polyvalent cation-sensing receptor precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Accession: 02-Ju-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
Db 115 VAQNKKDSNLNDEFNCNSEHIPSITIAVGATSGVSTAVANLGLFYIPQVSASSRL 174  
Qy 135 LTQGB--EIRPNERNSTGAFPA--GIVAGGGSFLSVPSARLGLYLYLPOGVYTSTCVIL 189  
Db 115 VAQNKKDSNLNDEFNCNSEHIPSITIAVGATSGVSTAVANLGLFYIPQVSASSRL 174  
Qy 190 SDKYQFPSPYLVIASDKIOSKAVVKRICHF 219

Db 175 SNKQPKSFSLRTLPNDHQATAMADIEYF 204

A:Accession: S40476

A;Status: preliminary

A;Molecule type: mRNA

A;Cross-references: UNIPROT: P215384; GB:S67307; PID:9453108

C;Species: Bos primigenius taurus (cattle)

C;Accession: S10476

R;Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butteri, R.; Kifor, O.; Sun, A.; H

Nature 366, 575-580, 1993

A;Title: Cloning and characterization of an extracellular Ca (2+)-sensing receptor from b

A;Reference number: S40476; MUID:94077182; PMID:8255296

A;Accession: S40476

A;Status: preliminary

A;Molecule type: mRNA

A;Cross-references: UNIPROT: P215384; BRO

C;Species: Rat

C;Accession: 19-Mar-1997 #text\_change 09-Jul-2004

Db 115 VAQNKKDSNLNDEFNCNSEHIPSITIAVGATSGVSTAVANLGLFYIPQVSASSRL 174

Qy 135 LTQGB--EIRPNERNSTGAFPA--GIVAGGGSFLSVPSARLGLYLYLPOGVYTSTCVIL 189

Db 115 VAQNKKDSNLNDEFNCNSEHIPSITIAVGATSGVSTAVANLGLFYIPQVSASSRL 174

Qy 190 SDKYQFPSPYLVIASDKIOSKAVVKRICHF 219

Db 175 SNKQPKSFSLRTLPNDHQATAMADIEYF 204

RESULT 4

A:Accession: 15362 calcium/polyvalent cation-sensing receptor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Accession: 19-Mar-1997 #sequence\_revision 19-Mar-1997  
R;Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butteri, R.; Kifor, O.; Sun, A.; H  
Nature 366, 575-580, 1993  
A;Title: Cloning and characterization of an extracellular Ca (2+)-sensing receptor from b  
A;Reference number: S40476; MUID:94077182; PMID:8255296

Query Match 30.7%

Best Local Similarity 42.2%

Matches 38; Mismatches 73; Indels 6; Gaps 3;

Db 33 ILGGLFPSPYLVIASDKIOSKAVVKRICHF 219

Qy 53 LVIGGLFPDSRTIPANESI-LEPASAKCEGFNQFRMVKAMIMIKBNKRDILPNI 111

Db 33 ILGGLFPSPYLVIASDKIOSKAVVKRICHF 219

Qy 112 TLGQFPSPYLVIASDKIOSKAVVKRICHF 219

Db 33 ILGGLFPSPYLVIASDKIOSKAVVKRICHF 219

Qy 112 TLGQFPSPYLVIASDKIOSKAVVKRICHF 219

|  |  |  |
|--|--|--|
|  |  | C;Superfamily: metabotropic glutamate receptor 4<br>C;Species: G protein-coupled receptor; receptor; transmembrane   |
|  |  | P:1/24#Domain: signal sequence #status predicted <SIG>   |
|  |  | P:25-879#Product: metabotropic glutamate receptor subtype 3 #status predicted <TM1>  |
|  |  | F:577-599#Domain: transmembrane #status predicted <TM1>  |
|  |  | F:646-664#Domain: transmembrane #status predicted <TM2>  |
|  |  | F:683-709#Domain: transmembrane #status predicted <TM3>  |
|  |  | F:731-756#Domain: transmembrane #status predicted <TM4>  |
|  |  | F:770-791#Domain: transmembrane #status predicted <TM5>  |
|  |  | F:804-828#Domain: transmembrane #status predicted <TM6>  |
|  |  | F:829-847#Domain: transmembrane #status predicted <TM7>  |
|  |  | Query Match 20.6%; Score 234.5; DB 2; Length 879;<br>Best Local Similarity 31.5%; Pred. No. 8.1e-14;<br>Matches 57; Conservative 36; Mismatches 63; Indels 25; Gaps 5;   |
|  |  | Qy 53 LVIGGLPIDIERTIPANESTILEPASAKCCEGFNFQFR-FRMKAMHIMIKBINKRKDILPNI 111<br>Db 39 IVLGGIIPINNEKGKGTGEE-----ORGNEBDGQORLEAMLFAIDBKNDYLLPGV 89   |
|  |  | Qy 112 TLGYQIPLFDTC---FRTISKSYBAVLYVLTGQEENRPNFRNSTGAFP-----AGIVG 158<br>Db 90 KLGVHHLDTCSRDTYALEQSLSFVRASLTKVB--AEMCPDGDSYATOBNIPLLIAGVG 147  |
|  |  | Qy 159 AGGSFTPSVPASRLGJYLPRQVGTTCTVILSDKYQPSYSLRVIASDKIOSKAVKRIOH 218<br>Db 148 GSYSSTSIQVANLRLFQIPIQSYASTSAKULSDKSRTDYFAPTVEPDFQAKAMAEILRY 207  |
|  |  | Qy 219 F 219   |
|  |  | Db 208 F 208   |
|  |  | RESULT 7<br>JC2132<br>metabotropic glutamate receptor 5 A - human  |
|  |  | C;Species: Homo sapiens (man)<br>C;Date: 28-Aug-1985 #sequence_change 05-Jan-1996<br>C;Accession: JC2132   |
|  |  | R;Minakami, R.; Katsumi, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.<br>Biochim. Biophys. Res. Commun. 199, 1136-1143, 1994<br>A;Title: Molecular cloning and the functional expression of two isoforms of human<br>A;Reference number: JC2131; MUID:94197696; PMID:7908515<br>A;Accession: JC2132<br>A;Molecule type: mRNA<br>A;Residues: 1-1180 <MIN><br>C;Comment: This protein is coupled to guanine nucleotide binding proteins.<br>C;Keywords: G-protein; neurotransmitter; receptor; transmembrane protein |
|  |  | Query Match 21.0%; Score 239.5; DB 2; Length 1218;<br>Best Local Similarity 29.5%; Pred. No. 4.1e-14;<br>Matches 56; Conservative 46; Mismatches 57; Indels 31; Gaps 6;  |
|  |  | Qy 53 LVIGGLPIDIERTIPANESTILEPASAKC---EGENFORFRMKAMHIMIKBINKRKDIL 108<br>Db 51 IIGALGSVHQ--PSTIQV--AERKGGEVREPOYGIQ---VEAMFHFTLDRINSNPNL 102   |
|  |  | Qy 109 PNITLGQIPLFDTCF---TISKSYBAVLYVLTGQEENRPNFR---NSTGAFPA---GI 159<br>Db 103 PNITLGCEIRDSCWHSSVALEQSTIEFIRDSLISRTDDNKGTSRQWCHGMPPSQPPAT 162   |
|  |  | Qy 150 GAPPAGIVGAGGSFLSPVSPASRLGJYLPRQVGTTCTVILSDKYQPSYSLRVIASDKIOS 209<br>Db 163 KRPIAGVIGPQGSSSVAIQVNLLQLENFNPQIAYSATSDLSDTKLFKPLRVVPSDTLQA 222  |
|  |  | Qy 210 KAVVKRIOHF 219  |
|  |  | Db 223 RAIFDIVRY 232   |
|  |  | Query Match 19.9%; Score 227; DB 2; Length 1180;<br>Best Local Similarity 30.6%; Pred. No. 5.9e-13;<br>Matches 56; Conservative 44; Mismatches 59; Indels 24; Gaps 7;  |
|  |  | Qy 53 LVIGGLPIDIERTIPANESTILEPASAKC---EGENFORFRMKAMHIMIKBINKRKDIL 108<br>Db 35 IIGALGSVHQ--PSTIQV--AERKGGEVREPOYGIQ---VEAMFHFTLDRINSNPNL 86  |
|  |  | Qy 109 PNITLGQIPLFDTCF---TISKSYBAVLYVLTGQEENRPNFR---NSTGAFPA---GI 156<br>Db 803-827#Domain: transmembrane #status predicted <TM7>  |
|  |  | Query Match 19.9%; Score 227; DB 2; Length 1180;<br>Best Local Similarity 30.6%; Pred. No. 5.9e-13;<br>Matches 56; Conservative 44; Mismatches 59; Indels 24; Gaps 7;  |
|  |  | Qy 53 LVIGGLPIDIERTIPANESTILEPASAKC---EGENFORFRMKAMHIMIKBINKRKDIL 108<br>Db 35 IIGALGSVHQ--PSTIQV--AERKGGEVREPOYGIQ---VEAMFHFTLDRINSNPNL 86  |
|  |  | Qy 109 PNITLGQIPLFDTCF---TISKSYBAVLYVLTGQEENRPNFR---NSTGAFPA---GI 156<br>Db 803-827#Domain: transmembrane #status predicted <TM7>  |
|  |  | RESULT 6<br>JC71160<br>metabotropic glutamate receptor subtype 3 precursor - mouse   |
|  |  | C;Species: Mus musculus (house mouse)<br>C;Date: 04-Mar-2000 #sequence_change 11-May-2000<br>C;Accession: JC71160  |
|  |  | R;Minoshima, T.; Nakaniishi, S.<br>J. Biochem. 126, 889-896, 1999<br>A;Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3<br>A;Reference number: JC71160; PMID:20012997; PMID:10544282  |
|  |  | Qy 157 VGAGGSPFLSPVSPASRLGJYLPRQVGTTCTVILSDKYQPSYSLRVIASDKIOSKAVKVKRI 216<br>Db 147 IGPGSSESAVQVNLQLFNTPQIAVSATMDLSDTKLFKPMRVPVSDAQQRAMADIV 206  |
|  |  | Qy 217 QHP 219   |

Db 207 KRY 209

RESULT 8

JC2131 metabotropic glutamate receptor 5 B - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 05-Jan-1996  
C;Accession: JC2131 R/Makami, R.; Katsui, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.  
Biochem. Biophys. Res. Commun., 199, 1136-1143, 1994  
A;Title: Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor 5  
A;Reference number: JG2131; MUID:94197696; PMID:7908515  
A;Accession: JC2131  
A;Molecule type: mRNA

C;Comment: This protein is coupled to guanine nucleotide binding proteins.  
C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein.  
P:380-604/Domain: transmembrane #status predicted <TM1>  
P:617-637/Domain: transmembrane #status predicted <TM2>  
P:644-664/Domain: transmembrane #status predicted <TM3>  
P:794-794/Domain: transmembrane #status predicted <TM4>  
P:738-759/Domain: transmembrane #status predicted <TM5>  
P:773-794/Domain: transmembrane #status predicted <TM6>  
P:803-827/Domain: transmembrane #status predicted <TM7>

Query Match Score 19.9%; Best Local Similarity 30.6%; Matches 56; Conservative 44; Pred. No. 6.1e-13; Indels 59; Gaps 7;

Db 35 LVIGGLSPIDSRTPANESILEPAKCK---EGFNQFRERWKMAMHMIKEENKRKDIL 108  
Db 35 IIIGALFSVHQI---PTVDKVE---RKCQAVREYQIGR---YEAMLHTLERINSDPTIL 86

Qy 109 PNITLGQIIFDTCPF---TISKSVAFLVPLTGQEBENRPNR---NSTGAFPA---GI 156  
Db 87 PNITLGCEIRDSCWHSIAVALEQSIPRDLISSEEEBLVRCDGSSSFRSKKP1IVG 146

Qy 157 VAGGGSPLSVPSASRIGLTLPOGVXTSCTVLSDKYPSVYLRIASDKIOSKAVYKRI 216  
Db 147 IGPGSSSVAIQVNLLQLQFNIPQIAYSAATSMDSLSDKTLKYPNRRVPPSDAQARAMYDIV 206

Qy 217 QHF 219  
Db 207 KRY 209

RESULT 9

I49142 metabotropic glutamate receptor 9 - mouse  
C;Species: Mus musculus (house mouse)  
C;Accession: I49142  
R;Durovini, R.M.; Zhang, C.; Ramonell, K.  
J. Neurosci., 15, 3075-3083, 1995

A;Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb  
A;Reference number: I49142; MUID:95239344; PMID:7722646  
A;Accession: I49142  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-308 <RES>  
C;Genetics: mGluR8  
C;Superfamily: metabotropic glutamate receptor 4  
C;ProteinFamily: neurotransmitter receptor

Query Match Score 19.8%; Best Local Similarity 28.6%; Matches 59; Conservative 41; Pred. No. 6e-13; Indels 75; Gaps 5;

Db 21 FYWLTMMORTHSDEYANSIRLDG-----DILGGFFPVHAXGERGYPCGDRIKKEKG 72

Qy 77 SAKCEGENQFRERWKMAMHMIKEENKRKDILPNITLGQIIFDTCPFSTSKSVEAVLVFLT 136  
Db 73 IHLRE-----AMLYAIDQTNKDFDLSNTLGVRILDTCSRDTYALEQSUTFVQ 121

Qy 137 GQ-BENRPNFRNSTGAFP-----AGUVGAGGSFLSYSPASRILGGLYTLPOGVXTSTCV 187  
Db 122 ALIEKDASDVVKCANGDPPIFTEDKISSGIGAASSSIMVANILRLFKIPQIYSVASTAP 181

Qy 188 ILSDPKQFSPSYLTVIASDKIOSKAVV 213  
Db 182 ELSDNTRYDFFSRVPPPSYQADMV 207

RESULT 10

A12916 metabotropic glutamate receptor mGluR5 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A42916  
R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.  
J. Biol. Chem., 267, 13361-13368, 1992  
A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 co-expressed with mGluR1  
A;Reference number: A42916; MUID:9217054; PMID:1320017  
A;Accession: A42916  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1171 <ABE>  
A;Cross-references: UNIPROT: P31424; GB: D10891; PID: BAA01711.1; PMID: d100218  
A;Experimental source: brain  
C;Keywords: G protein-coupled receptor; transmembrane protein  
A;Note: sequence extracted from NCBI backbone (NCBInr: 107749; NCBI: 107750)

Query Match Score 224.5%; Best Local Similarity 30.2%; Pred. No. 1e-12; Indels 62; Mismatches 55; Gaps 6;

Db 53 LVIGGLSPIDSRTPANESILEPAKCK---EGFNQFRERWKMAMHMIKEENKRKDIL 108  
Db 35 IIIGALFSVHQI---PTVDKVE---RKCQAVREYQIGR---YEAMLHTLERINSDPTIL 86

Qy 109 PNITLGQIIFDTCPF---TISKSVAFLVPLTGQEBENRPNR---NSTGAFPA---GI 156  
Db 87 PNITLGCEIRDSCWHSIAVALEQSIPRDLISSEEEBLVRCDGSSSFRSKKP1IVG 146

Qy 158 GAGGGSPLSVPSASRIGLTLPOGVXTSCTVLSDKYPSVYLRIASDKIOSKAVYKRI 217  
Db 147 GPGSSSVAIQVNLLQLQFNIPQIAYSAATSMDSLSDKTLKYPNRRVPPSDAQARAMYDIV 206

Qy 218 HF 219  
Db 207 RY 208

RESULT 11

JH0563 metabotropic glutamate receptor 4 precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: JH0563; I58149  
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.  
Neuron, 8, 169-179, 1992  
A;Title: A family of metabotropic glutamate receptors  
A;Reference number: JH0563  
A;Molecule type: mRNA  
A;Residues: 1-912 <TAN>

A;Cross-references: UNIPROT: P31423  
A;Experimental source: brain  
R;O'Hara, P.J.; Shepard, P.O.; Thogersen, H.; Venezia, D.; Haldeman, B.A.; McGrawe, V.; Neuron 11, 41-52, 1993



Biochem. Biophys. Res. Commun. 283, 236-242, 2001  
 A;Title: Molecular identification of a candidate receptor gene for sweet taste.

A;Contents: tongue  
 A;Accession: JC7633

A;Molecule type: mRNA

A;Residues: 1-158 <KIT>

C;Cross-references: UNIPROT:Q91VA4; DDBJ:AB049994

C;Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the sweet taste.

A;Gene: tir3

A;Map position: 4

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: transmembrane protein

Query Match Score 19.1%; DB 2; Length 858;  
 Best Local Similarity 30.8%; Pred. No. 3.2e-12;  
 Matches 52; Conservative 36; Mismatches 78; Indels 3; Gaps 2;  
 Qy 54 VIGGLFPDPDSRTIPANESSILBPASAKCEGFNFQRFRWMKAMIRMIKEINKRDILPNITL 113  
 Db 36 IUGGLFPFGSTEATLNQTNPNSIFCNRFSPGLFLAMAMKMAVEINGSALLPGRL 95  
 Qy 114 GYLEDFTPTISKRSVEAVLVFLTG-QEENRNRNFRNSTGAPP--AGIVGAGGSFLSVPAR 170  
 Db 96 GYDLEDTSSEPVPTVMTKSSLMFLAKYGQSISIAYCNYTQOPRVLAVIGPHSSELALITGK 155  
 Qy 171 ILGDIYLPQYGTSTCVLSDPKYQFSYSLRVIASDKIQSCAVKRIQHF 219  
 Db 156 FPPSFMLPQVSYTASMDRLSDRETFPSFVTPSDRVQLQAVVTLQNF 204

## RESULT 15

A1939  
 G protein-coupled glutamate receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Accession: A41939; S15362

R;Houamed, K.M.; Kuijper, J.L.; Gilbert, T.B.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill,

A;Title: Cloning, expression, and gene structure of a G protein-coupled glutamate receptor

A;Reference number: A41939; MUID:92022526; PMID:1656724

A;Accession: A41939

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-119 <HOUS>

A;Cross-references: UNIPROT:P23385; GB:M61099; NID:9397806; PID:AAA19497.1; PID:g204460

A;Experimental source: cerebellum

A;Note: Sequence extracted from NCBI backbone (NCBIP\_60785)

R;Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.

A;Title: Sequence and expression of a metabotropic glutamate receptor.

A;Reference number: S15362; MUID:91156047; PMID:1847995

A;Accession: S15362

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-119 <MAS>

A;Cross-references: EMBL:X57569; PID:956646; PID:CAA40799.1; PID:956647

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match Score 18.9%; DB 2; Length 1199;  
 Best Local Similarity 30.3%; Pred. No. 8.2e-12;  
 Matches 56; Conservative 42; Mismatches 57; Indels 30; Gaps 8;  
 Qy 53 LVIGGLFPDORTIPANESSILBPASAKC---EGENFORFRNMKAMIMIKERKNDIL 108  
 Db 45 VIIGAIFSTVHQ--PPAEVKPE--RKCGEBIRQYQGIOR--YEAMHTLDKINADPVL 96  
 Qy 109 PNITDGYQIFDTCF ---TIDSKEVEAV--LVFLGQEBENRPNFRNSTGAPP----- 153  
 Db 97 PNITDGYQIFDTCF ---TIDSKEVEAV--LVFLGQEBENRPNFRNSTGAPP----- 156

Qy 154 AGIVGAGGGFLSVPAASRLIGLYLPLQVGTYTSTCVLSDKQPSYLRVIASKA- 211

Db 157 AGVCPGSSSAVIOVQNLQLQFDIFQIAVSATSISSLDTLYKVRWPSDTRQARAML 216  
 Qy 212 -VVKR 215  
 Db :|||  
 217 DRIVER 221

Search completed: February 16, 2005, 16:37:52  
 Job time : 10.0413 SECS